



results of BLAST

BLASTP 2.2.5 [Nov-16-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1046895000-05007-6664

Query=

(1469 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

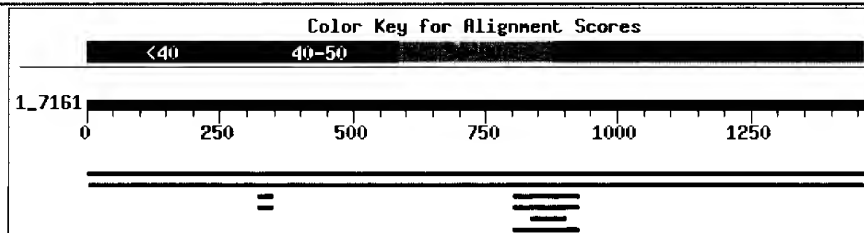
1,348,542 sequences; 431,791,111 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 8 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:					Score (bits)	E Value	
gi	23396465	sp	Q961D9	BCL9 DROME Bcl-9 homolog (Legless pro...	2076	0.0	L
gi	19550445	gb	AAL91368.1	AF457205_1 legless [Drosophila me...	2069	0.0	
gi	8132999	gb	AAF73447.1	AF263836_1 voltage-gated potassium...	39	0.58	L
gi	23593633	ref	XP_129704.2	potassium voltage-gated channe...	39	0.62	
gi	27672780	ref	XP_224941.1	similar to MAP/microtubule aff...	37	3.0	
gi	23396460	sp	O00512	BCL9 HUMAN B-cell lymphoma 9 protein ...	36	6.0	
gi	4757846	ref	NP_004317.1	B-cell CLL/lymphoma 9 [Homo sap...	36	6.2	L
gi	26328813	dbj	BAC28145.1	unnamed protein product [Mus mu...	35	9.5	

Alignments

Get selected sequences

Select all

Deselect all

>gi|23396465|sp|Q961D9|BCL9 DROME Bcl-9 homolog (Legless protein)
 gi|22759407|gb|AAF59345.2| CG2041-PA [Drosophila melanogaster]
 gi|21356901|ref|NP_651922.1| CG2041-PA [Drosophila melanogaster]
 gi|15291613|gb|AAK93075.1| **L** LD02061p [Drosophila melanogaster]
 Length = 1469

Score = 2076 bits (5379), Expect = 0.0

Identities = 1260/1469 (85%), Positives = 1260/1469 (85%)

Query: 1 MLSTTMPRSPTQQQPQXXXXXXXXXXXXXXXXXXXXXIGNGDSAASRSSPKTLNSEPFSTLSP 60
 MLSTTMPRSPTQQQPQ IGNGDSAASRSSPKTLNSEPFSTLSP
 Sbjct: 1 MLSTTMPRSPTQQQPQNSDASSTASGSNPGAAIGNGDSAASRSSPKTLNSEPFSTLSP 60

 Query: 61 DQIKLTPEEGTEKSGSLSTSDKAATGGAPGSGNNLPEGQTMLRQNSTSTINSLVAXXXXXX 120
 DQIKLTPEEGTEKSGSLSTSDKAATGGAPGSGNNLPEGQTMLRQNSTSTINSLVA
 Sbjct: 61 DQIKLTPEEGTEKSGSLSTSDKAATGGAPGSGNNLPEGQTMLRQNSTSTINSLVASPQNS 120

 Query: 121 XXXXXXXXXXXATVGLTQMVDCEQSKKNKCSVKDEEAEISSNKAQGAAAGGGCETGSTSS 180
 ATVGLTQMVDCEQSKKNKCSVKDEEAEISSNKAQGAAAGGGCETGSTSS
 Sbjct: 121 SEHSNSSNVSATVGLTQMVDCEQSKKNKCSVKDEEAEISSNKAQGAAAGGGCETGSTSS 180

 Query: 181 LTVKEEPTDVLGSLVNMKKEERENHSPTMSPVGFSGIGNAQDNSATPVKIERISNDSTTE 240
 LTVKEEPTDVLGSLVNMKKEERENHSPTMSPVGFSGIGNAQDNSATPVKIERISNDSTTE
 Sbjct: 181 LTVKEEPTDVLGSLVNMKKEERENHSPTMSPVGFSGIGNAQDNSATPVKIERISNDSTTE 240

 Query: 241 KKGSSLTMNNDMSMEGCNQLNPDFINESLNNPAISSILVXXXXXXXXXXXXXXXXXNLLT 300
 KKGSSLTMNNDMSMEGCNQLNPDFINESLNNPAISSILV NLLT
 Sbjct: 241 KKGSSLTMNNDMSMEGCNQLNPDFINESLNNPAISSILVSGVGPIPIGIVGAGTGNLLT 300

 Query: 301 XXXXXXXXXXXCLDYMQQQNHI FVFSTQLANKGAESVLSGQFQTIIAYHCTQPATKSFL 360
 CLDYMQQQNHI FVFSTQLANKGAESVLSGQFQTIIAYHCTQPATKSFL
 Sbjct: 301 ANANGISSGSSNCLDYMQQQNHI FVFSTQLANKGAESVLSGQFQTIIAYHCTQPATKSFL 360

 Query: 361 EDFFMKNPLKINKLQRHNSVGMPWIGMQVGLTPPNPVAKITQQQPHTKTVGLLKPQFNQ 420
 EDFFMKNPLKINKLQRHNSVGMPWIGMQVGLTPPNPVAKITQQQPHTKTVGLLKPQFNQ
 Sbjct: 361 EDFFMKNPLKINKLQRHNSVGMPWIGMQVGLTPPNPVAKITQQQPHTKTVGLLKPQFNQ 420

 Query: 421 HENSKRSTVSAPSNSFVDQSDPMGNETELMCWEGGSSNTRSNGQNSRNHVDSISTSSSEQ 480
 HENSKRSTVSAPSNSFVDQSDPMGNETELMCWEGGSSNTRSNGQNSRNHVDSISTSSSEQ
 Sbjct: 421 HENSKRSTVSAPSNSFVDQSDPMGNETELMCWEGGSSNTRSNGQNSRNHVDSISTSSSEQ 480

 Query: 481 AIKILEAAGVDLGQVTKGSDPGLTTENNIVSLQGVKVPDENLTPQQRQHREEQLAKIKKM 540
 AIKILEAAGVDLGQVTKGSDPGLTTENNIVSLQGVKVPDENLTPQQRQHREEQLAKIKKM
 Sbjct: 481 AIKILEAAGVDLGQVTKGSDPGLTTENNIVSLQGVKVPDENLTPQQRQHREEQLAKIKKM 540

 Query: 541 NQFLFPENENSVGANVSSQITKIPGDLXXXXXXXXXXXXXIIINPTMRQLHMPGNAKSELLSA 600
 NQFLFPENENSVGANVSSQITKIPGDL IINPTMRQLHMPGNAKSELLSA
 Sbjct: 541 NQFLFPENENSVGANVSSQITKIPGDLMMGMSGGGGSIINPTMRQLHMPGNAKSELLSA 600

 Query: 601 TSSGLSEDVMHPGDVISDMGAVIGCNNNQKTSVQCGSXXXXXXXXXXXXXXXXXMHCSSSG 660
 TSSGLSEDVMHPGDVISDMGAVIGCNNNQKTSVQCGS MHCSSSG
 Sbjct: 601 TSSGLSEDVMHPGDVISDMGAVIGCNNNQKTSVQCGSGVGVTGTTAAGVNVNMHCSSSG 660

 Query: 661 APNGNMMGSSTDMLASFGNTSCNVIGTAPDMSKEVLNQDSRTHSHQGGVAQMEWSKIQHQ 720
 APNGNMMGSSTDMLASFGNTSCNVIGTAPDMSKEVLNQDSRTHSHQGGVAQMEWSKIQHQ
 Sbjct: 661 APNGNMMGSSTDMLASFGNTSCNVIGTAPDMSKEVLNQDSRTHSHQGGVAQMEWSKIQHQ 720

 Query: 721 FFEERLKGKXXXXXXXXXXXXXXXXXSGSGGNSLNNQVRPLQGPPPPYHSIQRSASVPIAT 780
 FFEERLKGK SGSGGNSLNNQVRPLQGPPPPYHSIQRSASVPIAT
 Sbjct: 721 FFEERLKGKPRQVTGTVPQQQTPSGSGGNSLNNQVRPLQGPPPPYHSIQRSASVPIAT 780

 Query: 781 QXXXXXXXXXXXXXXXXRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSA 840
 Q RTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSA
 Sbjct: 781 QSPNPSSPNLPSLPSRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSA 840

Query: 841 NKNCFQADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSPKEFESFGQSSAGDNMK 900
 Sbjct: 841 NKNCFQADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSPKEFESFGQSSAGDNMK 900

Query: 901 SRRPSPQGQRSPVNSLIEANKDVRFAASSPGFNPHPHMQSNSNSALNAYKMGSTNIQMER 960
 Sbjct: 901 SRRPSPQGQRSPVNSLIEANKDVRFAASSPGFNPHPHMQSNSNSALNAYKMGSTNIQMER 960

Query: 961 QASAQGGSVQFSRRSDNIPLNPNSGNRPPPNKMTQNFDPISSLAQMSQQLTSCVXXXXXX 1020
 Sbjct: 961 QASAQGGSVQFSRRSDNIPLNPNSGNRPPPNKMTQNFDPISSLAQMSQQLTSCVSSMGSP 1020

Query: 1021 XXXXXXXXXXXXXXXDINIEHXXXXXXXXXXXXXXXXXNQNNCHSMNVVMNSMGPRMLNPKMC 1080
 Sbjct: 1021 AGTGGMTMMGGPGPSDINIEHGIISGLDGSIDTINQNNCHSMNVVMNSMGPRMLNPKMC 1080

Query: 1081 VAXXXXXXXXXXXXXXXXXXLRENSIGSGCGSANSSNFQGVVPPGARMGMMPVNFSGSNFN 1140
 Sbjct: 1081 VAGGPNGPPGFNPNSPNGGLRENSIGSGCGSANSSNFQGVVPPGARMGMMPVNFSGSNFN 1140

Query: 1141 PNIQVKASTPNTIQYMPVRAQXXXXXXXXXXXXXVRMPPSLEFLQRYANPQMGAVNGSGPI 1200
 Sbjct: 1141 PNIQVKASTPNTIQYMPVRAQANNNNNNGANNVRMPPSLEFLQRYANPQMGAVNGSGPI 1200

Query: 1201 CPPSASDGTXXXXXXXXXXXXXXXXXNSSGEQHQNKITNNPGASNGINFFQNCNQMSIVD 1260
 Sbjct: 1201 CPPSASDGTGMPGLMAGPGAGGMLNSSGEQHQNKITNNPGASNGINFFQNCNQMSIVD 1260

Query: 1261 EEGGLPGHDGSMNIGQPSMIRGMRPHAMRPNVMGARMPPVNRQIQFAQSSDGIDCVGDPS 1320
 Sbjct: 1261 EEGGLPGHDGSMNIGQPSMIRGMRPHAMRPNVMGARMPPVNRQIQFAQSSDGIDCVGDPS 1320

Query: 1321 SFFTNASCSNAGPHMFGSAQQANQPKTQHIKNIPSGMCQNQSGLAVAQGGQIQHLHGQGHQAQ 1380
 Sbjct: 1321 SFFTNASCSNAGPHMFGSAQQANQPKTQHIKNIPSGMCQNQSGLAVAQGGQIQHLHGQGHQAQ 1380

Query: 1381 GQSLIGPTNNNLMSTAGSVSATNGVSGINFGPSSTDLYAQQYHSFQQQLYATNTRSXX 1440
 Sbjct: 1381 GQSLIGPTNNNLMSTAGSVSATNGVSGINFGPSSTDLYAQQYHSFQQQLYATNTRSQQ 1440

Query: 1441 XXXXXXXXSNMITMPPNLSNPNTFFVNK 1469
 Sbjct: 1441 QQHMHQQHQSNNMITMPPNLSNPNTFFVNK 1469

>gi|19550445|gb|AAL91368.1|AF457205.1 legless [Drosophila melanogaster]
 Length = 1464

Score = 2069 bits (5360), Expect = 0.0
 Identities = 1255/1464 (85%), Positives = 1255/1464 (85%)

Query: 6 MPRSPTQQQPQXXXXXXXXXXXXXXXXXIGNGDSAASRSSPKTLNSEPFSTLSPDQIKL 65
 Sbjct: 1 MPRSPTQQQPQIGNGDSAASRSSPKTLNSEPFSTLSPDQIKL 60

Query: 66 TPEGTEKSGLSTSDKAATGGAPGSGNNLPEGQTMLRQNSTSTINSCLVAXXXXXXXXXXX 125
 Sbjct: 61 TPEGTEKSGLSTSDKAATGGAPGSGNNLPEGQTMLRQNSTSTINSCLVASPQNSSEHSN 120

Query: 126 XXXXXATVGLTQMVDCEQSKKNKCSVKDEEAEISSNKAQQAAGGGCETGSTSSLTVKE 185
 Sbjct: 121 SSVSATVGLTQMVDCEQSKKNKCSVKDEEAEISSNKAQQAAGGGCETGSTSSLTVKE 180

Query: 186 EPTDVLGSLVNMKKEERENHSPTMSPVGFGSIGNAQDNSATPVKIERISNDSTTEKKGSS 245
 Sbjct: 181 EPTDVLGSLVNMKKEERENHSPTMSPVGFGSIGNAQDNSATPVKIERISNDSTTEKKGSS 240

Query: 246 LTMNNDMSMEGCNQLNPDFINESLNNPAISSILVXXXXXXXXXXXXXXXXXNLLTXXXXX 305
 LTMNNDMSMEGCNQLNPDFINESLNNPAISSILV NLLT
 Sbjct: 241 LTMNNDMSMEGCNQLNPDFINESLNNPAISSILVSGVGPIPGIGVGAGTGNNLTANANG 300

Query: 306 XXXXXXCLDYMQQQNHIFVFSTQLANKGAESVLSGQFQTIIAYHCTQPATKSFLEDDFFM 365
 CLDYMQQQNHIFVFSTQLANKGAESVLSGQFQTIIAYHCTQPATKSFLEDDFFM
 Sbjct: 301 ISSGSSNCLDYMQQQNHIFVFSTQLANKGAESVLSGQFQTIIAYHCTQPATKSFLEDDFFM 360

Query: 366 KNPLKINKLQRHNSVGMPWIGMGQVGLTPPNPAKITQQQPHTKTVGLLKPQFNQHENS 425
 KNPLKINKLQRHNSVGMPWIGMGQVGLTPPNPAKITQQQPHTKTVGLLKPQFNQHENS
 Sbjct: 361 KNPLKINKLQRHNSVGMPWIGMGQVGLTPPNPAKITQQQPHTKTVGLLKPQFNQHENS 420

Query: 426 RSTVSAPSNSFVDQSDPMGNETELMCWEGGSSNTSRSGQNSRNHVDSISTSSSESQAIKIL 485
 RSTVSAPSNSFVDQSDPMGNETELMCWEGGSSNTSRSGQNSRNHVDSISTSSSESQAIKIL
 Sbjct: 421 RSTVSAPSNSFVDQSDPMGNETELMCWEGGSSNTSRSGQNSRNHVDSISTSSSESQAIKIL 480

Query: 486 EAAGVDLGQVTKGSDPGLTTENNIVSLQGKVPDENLTPQQRQHREEQLAKIKKMNQFLF 545
 EAAGVDLGQVTKGSDPGLTTENNIVSLQGKVPDENLTPQQRQHREEQLAKIKKMNQFLF
 Sbjct: 481 EAAGVDLGQVTKGSDPGLTTENNIVSLQGKVPDENLTPQQRQHREEQLAKIKKMNQFLF 540

Query: 546 PENENSVGANVSSQITKIPGDLXXXXXXXXXXIINPTMRQLHMPGNAKSELLSATSSGL 605
 PENENSVGANVSSQITKIPGDL IINPTMRQLHMPGNAKSELLSATSSGL
 Sbjct: 541 PENENSVGANVSSQITKIPGDLMMGMSGGGGSIINPTMRQLHMPGNAKSELLSATSSGL 600

Query: 606 SEDVMHPGDVISDMGAVIGCNNNQKTSVQCGSXXXXXXXXXXXXXXXXXMHCSSSGAPNGN 665
 SEDVMHPGDVISDMGAVIGCNNNQKTSVQCGS MHCSSSGAPNGN
 Sbjct: 601 SEDVMHPGDVISDMGAVIGCNNNQKTSVQCGSGVGVTGTAAAGVNVNMHCSSGAPNGN 660

Query: 666 MMGSSTDMLASFGNTSCNVIGTAPDMSKEVLNQDSRTHSHQGGVAQMEWSKIQHQQFEER 725
 MMGSSTDMLASFGNTSCNVIGTAPDMSKEVLNQDSRTHSHQGGVAQMEWSKIQHQQFEER
 Sbjct: 661 MMGSSTDMLASFGNTSCNVIGTAPDMSKEVLNQDSRTHSHQGGVAQMEWSKIQHQQFEER 720

Query: 726 LKGGKXXXXXXXXXXXXXXXXXSGSGGNSLNNQVRPLQGPPPPYHSIQRSASVPIATQXXXX 785
 LKGGK SGSGGNSLNNQVRPLQGPPPPYHSIQRSASVPIATQ
 Sbjct: 721 LKGGKPRQVTGTVPQQTPSGSGGNSLNNQVRPLQGPPPPYHSIQRSASVPIATQSPNP 780

Query: 786 XXXXXXXXXXXRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSANKNCF 845
 RTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSANKNCF
 Sbjct: 781 SSPNNLSLPSRRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSANKNCF 840

Query: 846 QADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSPKEFESFGQSSAGDNMKSRRPS 905
 QADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSPKEFESFGQSSAGDNMKSRRPS
 Sbjct: 841 QADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSPKEFESFGQSSAGDNMKSRRPS 900

Query: 906 PQGQRSPVNSLIEANKDVRFAASSPGFNPHPHMQSNSNSALNAYKMGSTNIQMERQASAQ 965
 PQGQRSPVNSLIEANKDVRFAASSPGFNPHPHMQSNSNSALNAYKMGSTNIQMERQASAQ
 Sbjct: 901 PQGQRSPVNSLIEANKDVRFAASSPGFNPHPHMQSNSNSALNAYKMGSTNIQMERQASAQ 960

Query: 966 GGSVQFSRRSDNIPLNPNSGNRPPPNKMTQNFDPISSLAQMSQQLTSCVXXXXXXXXXXXX 1025
 GGSVQFSRRSDNIPLNPNSGNRPPPNKMTQNFDPISSLAQMSQQLTSCV
 Sbjct: 961 GGSVQFSRRSDNIPLNPNSGNRPPPNKMTQNFDPISSLAQMSQQLTSCVSSMGSPAGTGG 1020

Query: 1026 XXXXXXXXXXXDINIEHXXXXXXXXXXXXXXXXXNQNCHSMNVVMNSMGPRMLNPKMCVAXXX 1085
 DINIEH NQNCHSMNVVMNSMGPRMLNPKMCVA
 Sbjct: 1021 MTMMGGPGPSDINIEHGISGLDGSIDTINQNCHSMNVVMNSMGPRMLNPKMCVAGGP 1080

Query: 1086 XXXXXXXXXXXXXXXLRENSIGSGCGSANSSNFQGVVPPGARMMPVNFSGSNFNPNIQV 1145
 LRENSIGSGCGSANSSNFQGVVPPGARMMPVNFSGSNFNPNIQV
 Sbjct: 1081 NGPPGFNPNSPNGGLRENSIGSGCGSANSSNFQGVVPPGARMMPVNFSGSNFNPNIQV 1140

Query: 1146 KASTPNTIQYMPVRAQXXXXXXXXXXXXXVRMPPSLEFLQRYANPQMGA VNGSPICPPSA 1205
 KASTPNTIQYMPVRAQ VRMPPSLEFLQRYANPQMGA VNGSPICPPSA
 Sbjct: 1141 KASTPNTIQYMPVRAQANNNNNNNGANNVRMPPSLEFLQRYANPQMGA VNGSPICPPSA 1200

Query: 1206 SDGTXXXXXXXXXXXXXXXXXNSSGEQHQNKITNNPGASNGINFFQNCNQMSIVDEEGGL 1265
 SDGT NSSGEQHQNKITNNPGASNGINFFQNCNQMSIVDEEGGL
 Sbjct: 1201 SDGTPGMPGLMAGPGAGGMLMNSSGEQHQNKITNNPGASNGINFFQNCNQMSIVDEEGGL 1260

Query: 1266 PGHDGSMNIGQPSMIRGMRPHAMRPNVMGARMPPVNRQIQFAQSSDGIDCVGDPSSFFTN 1325
 PGHDGSMNIGQPSMIRGMRPHAMRPNVMGARMPPVNRQIQFAQSSDGIDCVGDPSSFFTN
 Sbjct: 1261 PGHDGSMNIGQPSMIRGMRPHAMRPNVMGARMPPVNRQIQFAQSSDGIDCVGDPSSFFTN 1320

Query: 1326 ASCNSAGPHMFGSAQQANQPKTQHIKNIPSGMCQNQSGLAVAQGGIQLHGQGHAAQQSLI 1385
 ASCNSAGPHMFGSAQQANQPKTQHIKNIPSGMCQNQSGLAVAQGGIQLHGQGHAAQQSLI
 Sbjct: 1321 ASCNSAGPHMFGSAQQANQPKTQHIKNIPSGMCQNQSGLAVAQGGIQLHGQGHAAQQSLI 1380

Query: 1386 GPTNNNLMTAGSVSATNGVSGINFGPSSTDLKYAQQYHSFQQQLYATNTRSDXXXXXXX 1445
 GPTNNNLMTAGSVSATNGVSGINFGPSSTDLKYAQQYHSFQQQLYATNTRSD
 Sbjct: 1381 GPTNNNLMTAGSVSATNGVSGINFGPSSTDLKYAQQYHSFQQQLYATNTRSDQQQHM 1440

Query: 1446 XXXXSNMITMPPNLSNPPTFFVNK 1469
 SNMITMPPNLSNPPTFFVNK
 Sbjct: 1441 QQHQSNMITMPPNLSNPPTFFVNK 1464

>gi|8132999|gb|AAF73447.1|AF263836.1 voltage-gated potassium channel KCNQ5 [Mu
 gi|14285398|sp|Q9JK45|CIQ5 MOUSE Potassium voltage-gated channel subfamily KQT me
 channel KQT-like 5)
 Length = 878

Score = 38.9 bits (89), Expect = 0.58
 Identities = 34/138 (24%), Positives = 65/138 (47%), Gaps = 14/138 (10%)

Query: 806 PTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSANK---NCFQADTPSPSNQNR---S 858
 P +S + G+ SG + ++ ++ + G +L+ N+ F A +P+ +Q S
 Sbjct: 606 PVDSKDLGSAQNSGCLTRSASANISRLQFILTPNEFSAQTFYALSPTMHSQATQVPMS 665

Query: 859 RNTGSSSVLTHNLSSN-----PSTPLSHLSPKEFESFGQSSAGDNMKSRRPSPQGQRSP 912
 +N GSS V T+N+++ P+ P + P + S + + S Q S
 Sbjct: 666 QNDGSSVATNNIANQISAAPKPAAPTTLQIPPLSAIKHLSRPEPLLSNPGLQESISD 725

Query: 913 VNSLIEANKD-VRFAASS 929
 V + + A+K+ V+FA S+
 Sbjct: 726 VTTCLVASKESVQFAQSN 743

>gi|23593633|ref|XP_129704.2| potassium voltage-gated channel, subfamily Q, memb
 musculus]
 Length = 846

Score = 38.9 bits (89), Expect = 0.62
 Identities = 34/138 (24%), Positives = 65/138 (47%), Gaps = 14/138 (10%)

Query: 806 PTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSANK---NCFQADTPSPSNQNR---S 858
 P +S + G+ SG + ++ ++ + G +L+ N+ F A +P+ +Q S
 Sbjct: 574 PVDSKDLGSAQNSGCLTRSASANISRLQFILTPNEFSAQTFYALSPTMHSQATQVPMS 633

Query: 859 RNTGSSSVLTHNLSSN-----PSTPLSHLSPKEFESFGQSSAGDNMKSRRPSPQGQRSP 912
 +N GSS V T+N+++ P+ P + P + S + + S Q S
 Sbjct: 634 QNDGSSVATNNIANQISAAPKPAAPTTLQIPPLSAIKHLSRPEPLLSNPGLQESISD 693

Query: 913 VNSLIEANKD-VRFAASS 929
 V + + A+K+ V+FA S+
 Sbjct: 694 VTTCLVASKESVQFAQSN 711

>gi|27672780|ref|XP_224941.1| similar to MAP/microtubule affinity-regulating kir
 ELKL motif kinase 1; ELKL motif kinase [Homo sapiens]
 [Rattus norvegicus]
 Length = 654

Score = 36.6 bits (83), Expect = 3.0

Identities = 18/68 (26%), Positives = 33/68 (48%), Gaps = 8/68 (11%)



Query: 838 LSANKNCFQADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSPKEFESFGQSSAGD 897
 +S NCF N++ S N G +++ H + ++P+ + P+ +SFG SA +
 Sbjct: 421 ISPTLNCF-----NKSESLNKGKRTIVRHTMPPKKTSPVRRICPRLHKSFSGMGSASE 472

Query: 898 NMKSRRPS 905
 + R S
 Sbjct: 473 DSSKRNSS 480

gi|23396460|sp|O00512|BCL9_HUMAN B-cell lymphoma 9 protein (Bcl-9) (Legless hom
 Length = 1426

Score = 35.8 bits (81), Expect = 6.0
 Identities = 16/28 (57%), Positives = 25/28 (89%)

Query: 323 IFVFSTQLANKGAESVLSGQFQTIIAYH 350
 ++VFST++ANK AE+VL GQ +TI+++H
 Sbjct: 177 VYVFSTEMANKAAEAVLKGQVETIVSFH 204

gi|4757846|ref|NP_004317.1|  B-cell CLL/lymphoma 9 [Homo sapiens]
gi|2570024|emb|CAA73942.1|  B-cell CLL/lymphoma 9 [Homo sapiens]
 Length = 1394

Score = 35.8 bits (81), Expect = 6.2
 Identities = 16/28 (57%), Positives = 25/28 (89%)

Query: 323 IFVFSTQLANKGAESVLSGQFQTIIAYH 350
 ++VFST++ANK AE+VL GQ +TI+++H
 Sbjct: 177 VYVFSTEMANKAAEAVLKGQVETIVSFH 204

gi|26328813|dbj|BAC28145.1| unnamed protein product [Mus musculus]
 Length = 572

Score = 35.0 bits (79), Expect = 9.5
 Identities = 34/138 (24%), Positives = 65/138 (47%), Gaps = 14/138 (10%)

Query: 806 PTNSPSMDGTGSLSGSVPQANTSTVQAGTTTVLSANK---NCFQADTPSPSNQNR---S 858
 P +S + G+ SG + ++ ++ + G +L+ N+ F A +P+ +Q S
 Sbjct: 300 PVDSKDLSGSAQNSGCLTRSASANISRLQFILTPNEFSAQTFYALSPTMHSQATQVPMS 359

Query: 859 RNTGSSSVLTHNLSSN-----PSTPLSHLSPKEFESFGQSSAGDNMKSRRPSPQGQRSP 912
 +N GSS V T+N+++ P+ P + P + S + + S Q S
 Sbjct: 360 QNDGSSVATNNIANQISAAPKPAAPTTLQIPPLSAIKHLRPEPLLSNPTGLQESISD 419

Query: 913 VNSLIEANKD-VRFAASS 929
 V + + A+K+ V+FA S+
 Sbjct: 420 VTTCLVASKESVQFAQSN 437

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF
 Posted date: Feb 26, 2003 10:23 PM
 Number of letters in database: 431,791,111
 Number of sequences in database: 1,348,542

Lambda K H
 0.309 0.125 0.356

Gapped
 Lambda K H

0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1,110,058,764

Number of Sequences: 1348542

Number of extensions: 43687358

Number of successful extensions: 111049

Number of sequences better than 10.0: 267

Number of HSP's better than 10.0 without gapping: 24

Number of HSP's successfully gapped in prelim test: 258

Number of HSP's that attempted gapping in prelim test: 108537

Number of HSP's gapped (non-prelim): 1637

length of query: 1469

length of database: 431,791,111

effective HSP length: 136

effective length of query: 1333

effective length of database: 248,389,399

effective search space: 331103068867

effective search space used: 331103068867

T: 11

A: 40

X1: 16 (7.1 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 42 (21.7 bits)

S2: 79 (35.0 bits)